

L2 ANSWER 1 OF 1 MEDLINE
AN 91209917 MEDLINE
DN 91209917
TI Glucosyltransferase gene polymorphism among Streptococcus mutans strains.
AU Chia J S; Hsu T Y; Teng L J; Chen J Y; Hahn L J; Yang C S
CS School of Dentistry, National Taiwan University, Taipei, Republic of China..
SO INFECTION AND IMMUNITY, (1991 May) 59 (5) 1656-60.
Journal code: GO7. ISSN: 0019-9567.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199108
AB Genetic polymorphisms in genes coding for the glucosyltransferases were detected among Streptococcus mutans serotype c strains by Southern blot analysis with DNA probes located within the **gtfB gene** (H. Aoki, T. **Shiroza**, M. Hayakawa, S. Sato, and H. K. Kuramitsu, Infect. Immun. 53:587-594, 1986). Restriction endonucleases were used to examine genomic DNAs isolated from serotype a to h strains. The variations were readily detected among 33 strains of serotype c by EcoRI and PstI restriction enzyme digestions. Serotypes e and f, which are genetically similar to serotype c, also had comparable polymorphism; however, serotypes a, b, d, g, and h did not hybridize to the same DNA probes in parallel experiments. Further analysis of enzymatic activities for glucan synthesis and sucrose-dependent adherence revealed no significant differences among the serotype c strains. Our results suggested that genetic polymorphisms existing in S. mutans serotype c strains may reflect a complexity in genes coding for the glucosyltransferases, which are produced

 W O R L D
 (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

MSrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Jan 11 15:47:50 2000; Maspar time 2.45 Seconds
 234.053 Million cell updates/sec
 Tabu output not generated.

Title: >US-09-290-049-3
 Description: (1-22) from US94250049.pap
 Perfect Score: 155
 Sequence: 1 TGARTINGQLLYFRANGVQVKG 22

Scoring table:
 Gap 150
 PAM 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 29.681; Variance 38.978; scale 0.761

Prod. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Prod. No.
1	155	100.0	1475	1	GTFF_STRMU	9.19e+23
2	114	73.5	1597	1	GTFF1_STRDO	4.74e+12
3	114	72.3	1592	1	GTFF2_STRDO	1.49e+11
4	106	68.4	1375	1	GTFFC_STRMU	4.46e+10
5	104	67.1	1365	1	GTFFS_STRMU	1.36e+09
6	93	60.0	1430	1	GTFFD_STRMU	5.53e+07
7	79	51.0	382	1	YU07_YEAST	7.50e+04
8	72	45.5	126	1	DOC_BPPI	2.20e+02
9	70	46.2	529	1	Y119_NPPOP	5.58e+02
10	67	43.2	2710	1	TOXA_CLODI	2.19e+01
11	65	41.9	349	1	PTER_MOUSE	5.32e+01
12	65	41.9	1396	1	VLTF_BPT5	5.32e+01
13	63	40.6	301	1	LEC1_MOUSE	1.27e+00
14	63	40.6	310	1	YC08_PYRHO	1.27e+00
15	63	40.6	349	1	PTER_RAT	1.27e+00
16	63	40.6	396	1	DUT_VZVD	1.27e+00
17	63	40.6	404	1	CAG5_CHICK	1.27e+00
18	63	40.6	475	1	AP54_YEAST	1.27e+00
19	63	40.6	1082	1	RRPO_ROTFC	1.27e+00
20	62	40.0	464	1	VI2_HPV27	1.95e+00
21	62	40.0	467	1	ISP6_SCHPO	1.95e+00
22	62	40.0	524	1	VI2_HPV2A	1.95e+00
23	61	39.4	336	1	VINT_BP186	2.97e+00

RESULT ID	1	STANDARD	PR1	1475 AA
AC	01-NOV-1988 (REL. 09, CREATED)			
AD	P08987;			
DT	01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)			
DT	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)			
DE	GLUCOSYLTRANSFERASE-1 PRECURSOR (EC 2.4.1.5) (GTF-I) (DEXTRANSUCRASE) (SUCROSE 6-GLUCOSYLTRANSFERASE).			
GN	GTFF.			
OS	STREPTOCOCCUS MUTANS.			
OC	BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE; STREPTOCOCCUS.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-GS-5;			
RX	MEDLINE; 87308013.			
RA	SHIROGA T., UEDA S., KURAMITSU H.K.;			
RT	*Sequence analysis of the gtfb gene from Streptococcus mutans.*;			
RL	J. BACTERIOL. 163:4263-4270(1982).			
CC	- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIANE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.			
CC	- CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL) (N) -			
CC	- D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL) (N+1).			
CC	- SUBCELLULAR LOCATION: SECRETED.			
CC	- DISEASE: DENTAL CARIES.			
CC	- GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES). GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF GLUCANS.			
CC	- SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCAN-BINDING PROTEIN FROM S. MUTANS.			
CC	THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION - THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL ENTITIES REQUIRES A LICENSE AGREEMENT (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).			
CC	EMBL; M17361; G153640; -			
DR	PIR; B33135; B33135.			
DR	PFAM; PF00128; alpha-amyase; 1.			
KW	TRANSFERASE; GLUCOSYLTRANSFERASE; SIGNAL; REPEAT; DENTAL CARIES.			
FT	SIGNAL 1 34 POTENTIAL.			

FT CHAIN 35 1475 GLUCOSYLTRANSFERASE-I.
 FT DOMAIN 35 1050 CATALYTIC (APPROXIMATE).
 FT DOMAIN 1096 1475 GLUCAN-BINDING (APPROXIMATE).
 FT DOMAIN 1096 1129 A REPEAT.
 FT DOMAIN 1160 1469 5 X TANDEM REPEATS.
 FT REPEAT 1160 1209 1.
 FT REPEAT 1224 1274 2.
 FT REPEAT 1289 1339 3.
 FT REPEAT 1354 1404 4.
 FT REPEAT 1419 1469 5.
 SQ SEQUENCE 1475 AA; 165812 MM; 4542C1D6 CRC32;

Query Match 100.0%; Score 155; DB 1; Length 1475;
 Best Local Similarity 100.0%; Pred. No. 9,19e-23;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1300 TGAATIKGKLYKANGOVYK 1321
 OY 1 TGARTINGOLLYFRANGOVYK 22

RESULT 2
 ID GTF1_STRDO STANDARD; PRT: 1597 AA.
 AC 11001;
 DT 01-JUL-1989 (REL. 11, CREATED)
 DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE GLUCOSYLTRANSFERASE-1 PRECURSOR (EC 2.4.1.5) (GTF-1) (DEXTRANSUCRASE)
 DE (SUROSE 6-GLUCOSYLTRANSFERASE).
 GN GTF1.
 OS STREPTOCOCCUS DORNEI (STREPTOCOCCUS SOBRINUS).
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 RN STREPTOCOCCUS.
 RP (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-MFE28;
 RX MEDLINE: 87308014.
 RA FERRETI J.J., GILPIN M.L., RUSSELL R.R.B.;
 RT Nucleotide sequence of a glucosyltransferase gene from Streptococcus
 RT sobrinus Mfe28.*;
 RL J. BACTERIOL. 169:4271-4276(1987).
 CC -1- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
 CC TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
 CC OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIANE THE
 CC AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
 CC -1- CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) -
 CC D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- DISEASE: DENTAL CARIES.
 CC -1- GTF-1 SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED
 CC GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE
 CC GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF
 CC GLUCANS.
 CC -1- SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCAN-
 CC BINDING PROTEIN FROM S.MUTANS.

 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: M17391; G153647; -
 DR PIR: P00128; alpha-amylase; 1.
 KW TRANSFERASE: GLUCOSYLTRANSFERASE: SIGNAL; REPEAT; DENTAL CARIES.
 FT SIGNAL 1 38 POTENTIAL.
 FT CHAIN 39 1597 GLUCOSYLTRANSFERASE-1.
 FT DOMAIN 39 1050 CATALYTIC (APPROXIMATE).
 FT DOMAIN 1099 1597 GLUCAN-BINDING (APPROXIMATE).
 FT DOMAIN 1099 1597 1.25 A, 2 B, AND 5 AC REPEATS.
 FT REPEAT 1099 1132 A REPEAT.

FT REPEAT 1163 1213 AC REPEAT.
 FT REPEAT 1227 1277 AC REPEAT.
 FT REPEAT 1292 1342 AC REPEAT.
 FT REPEAT 1352 1399 B REPEAT.
 FT REPEAT 1406 1455 B REPEAT.
 FT REPEAT 1465 1512 AC REPEAT.
 FT REPEAT 1519 1568 B REPEAT.
 FT REPEAT 1582 1597 AC REPEAT.
 SQ SEQUENCE 1597 AA; 177080 MM; 995233CA CRC32;

Query Match 73.5%; Score 114; DB 1; Length 1597;
 Best Local Similarity 77.3%; Pred. No. 4,74e-12;
 Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 1303 TGAATIKGKLYKANGOVYK 1324
 OY 1 TGARTINGOLLYFRANGOVYK 22

RESULT 3
 ID GTF2_STRDO STANDARD; PRT: 1592 AA.
 AC P27470;
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE GLUCOSYLTRANSFERASE-1 PRECURSOR (EC 2.4.1.5) (GTF-1) (DEXTRANSUCRASE)
 DE (SUROSE 6-GLUCOSYLTRANSFERASE).
 OS STREPTOCOCCUS DORNEI (STREPTOCOCCUS SOBRINUS).
 OC BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
 RN STREPTOCOCCUS.
 RP (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-6715;
 RX MEDLINE: 91123227.
 RA ABO H., MATSUMURA T., KODAMA T., OHTA H., FUKUI K., KATO K.,
 RA KAGAWA H.;
 RT "Peptide sequences for sucrose splitting and glucan binding within
 RT Streptococcus sobrinus glucosyltransferase (water-insoluble glucan
 RT synthetase).";
 RL J. BACTERIOL. 173:989-996(1991).
 CC -1- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
 CC TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
 CC OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIANE THE
 CC AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
 CC -1- CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) -
 CC D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- DISEASE: DENTAL CARIES.
 CC -1- GTF-1 SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED
 CC GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE
 CC GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF
 CC GLUCANS.
 CC -1- SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCAN-
 CC BINDING PROTEIN FROM S.MUTANS.

 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: D90213; G217033; -
 DR PIR: A38175; A38175.
 KW TRANSFERASE: GLUCOSYLTRANSFERASE: SIGNAL; REPEAT; DENTAL CARIES.
 FT SIGNAL 1 38 POTENTIAL.
 FT CHAIN 39 1592 GLUCOSYLTRANSFERASE-1.
 FT DOMAIN 39 1044 CATALYTIC (APPROXIMATE).
 FT DOMAIN 1093 1592 GLUCAN-BINDING (APPROXIMATE).
 FT DOMAIN 1093 1592 6.5 X TANDEM REPEATS.